

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Nikolaus (Klaus) Theres
 (B) STREET: Schiffgesweg 30
 (C) CITY: Pulheim
 (D) STATE: NRW
 (E) COUNTRY: Germany
 (F) POSTAL CODE: 50259
 (G) TELEPHONE: + 49 2234 89386

(ii) TITLE OF INVENTION: PLANTS WITH CONTROLLED SIDE-SHOOT FORMATION
 AND/OR ABSCISSION ZONE FORMATION

(iii) NUMBER OF SEQUENCES: 14

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1729 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETIC: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon esculentum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

| | |
|--|-----|
| CCTCTGTCCT TCCCCCAGG TCCCCTTTTT TTCCTTTCTC TCTCTCCTTT ATTTCTCTTT | 60 |
| TCATAAGCAT ATTCTTTCTC TCTCTAGGGT TTTCACTTTC ACCTGAAATA GTGTTGTTAA | 120 |
| ATTGAATGAT ATGTTAGGAT CCTTTGGTTC TTCATCATCT CAATCTCACC CTCATCATGA | 180 |
| TGAAGAATCT TCTGATCATC ATCAACAGCG TAGATTCAACC GCTACTGCTA CAACTATCAC | 240 |
| CACCACCACC ATCACTACCT CACCAGCTAT TCAAATCCGC CAGCTACTCA TTAGCTGTGC | 300 |
| GGAGTTGATT TCGCAGTCCG ATTTCTCGGC CGCGAAAAGA CTCCTTACTA TATTATCAAC | 360 |
| TAACTCATCT CCTTTTGGTG ATTCAACTGA ACGGTTAGTC CATCAATTTA CTCGCGCACT | 420 |
| TTCCCTTCGT CTCAACCGCT ATATATCGTC AACCACCAAT CATTTTCATGA CACCTGTTGA | 480 |
| AACAACTCCA ACTGATTCTT CTTCTTCGTC ATCATTAGCT CTAATTCAAT CATCATATCT | 540 |
| ATCTCTAAAC CAAGTTACCC CTTTCATAAG GTTTACTCAA TTAACCGCTA ATCAAGCGAT | 600 |

003010"e9ee0460

TTTAGAAGCG ATTAACGGTA ATCATCAAGC AATCCACATC GTTGATTTTCG ACATTAATCA 660
 CGGGGTTCAA TGGCCACCGT TAATGCAAGC ACTAGCTGAT CGTTACCCTG CTCCCCTCT 720
 TCGAATCACC GGTACTGGAA ATGACCTTGA TACCCTTCGT AGAACAGGTG ATCGTTTAGC 780
 TAAATTTGCT CACTCATTAG GGTTGAGATT TCAATTCCAT CCTCTTTATA TAGCCAATAA 840
 TAACCACGAT CACGATGAAG ATCCTTCTAT TATTTCTCTC ATTGTACTAC TCCCTGATGA 900
 AACCTAGCT ATCAACTGTG TTTTCTACCT CCACCGCCTT TTAAGAGACC GCGAAAAGTT 960
 AAGGATTTTT TTGCATAGGG TTAAGTCAAT GAACCCTAAA ATTGTTACAA TCGCGGAGAA 1020
 GGAAGCAAAT CATAACCATC CTCTTTTTTT ACAAGATTC ATCGAGGCGT TGGATTATTA 1080
 TACAGCTGTG TTTGATTAC TGGAAGCTAC ATTGCCACCG GGTAGTCGAG AGAGGATGAC 1140
 AGTTGAACAA GTGTGGTTTG GGAGAGAGAT TGTTGATATC GTTGCGATGG AAGGAGATAA 1200
 AAGGAAAGAA AGACATGAAA GGTTTAGATC ATGGGAAGTT ATGTTGAGGA GTTGTGGATT 1260
 TAGTAATGTT GCTTTAAGCC CTTTTCGATT ATCACAAGCT AAGCTTCTTT TGAGACTTCA 1320
 TTATCCTTCT GAAGGCTATC AACTCGGAGT TTCGAGTAAT TCTTCTTCT TAGGTTGGCA 1380
 AAATCAACCC CTTTCTCCA TCTCGTCTTG GCGTTGAGAA AAATATCAA ATAGCCAAC 1440
 TCAGAGGGTA ATTAAGACTA CTGATAGTTT AGGAGGGATC TGAAGAAAAC GCGTGGAGTG 1500
 AAAACCTAA ATAACCAGAT TTTCTAATGA AGTTGTAGTA GTAGAAATTT GCATGGTGAA 1560
 GAACAATATT GAAGAGGTAT TGAAATTTCA TGTTTTTTTT GTTTTACTTA TTGATATGAA 1620
 TGTTTTAAAA TTTTAAACAT AGAGGACTAG GTTGATGATA TATAGTATTT AAGTTAACTA 1680
 GTCTTTGTAT AACGCAAGAT CTTGATCAAC TTATTTTAT TTTAATTA 1729

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Leu Gly Ser Phe Gly Ser Ser Ser Ser Gln Ser His Pro His His
 1 5 10 15
 Asp Glu Glu Ser Ser Asp His His Gln Gln Arg Arg Phe Thr Ala Thr
 20 25 30
 Ala Thr Thr Ile Thr Thr Thr Thr Ile Thr Thr Ser Pro Ala Ile Gln
 35 40 45
 Ile Arg Gln Leu Leu Ile Ser Cys Ala Glu Leu Ile Ser Gln Ser Asp
 50 55 60

Phe Ser Ala Ala Lys Arg Leu Leu Thr Ile Leu Ser Thr Asn Ser Ser
 65 70 75 80
 Pro Phe Gly Asp Ser Thr Glu Arg Leu Val His Gln Phe Thr Arg Ala
 85 90 95
 Leu Ser Leu Arg Leu Asn Arg Tyr Ile Ser Ser Thr Thr Asn His Phe
 100 105 110
 Met Thr Pro Val Glu Thr Thr Pro Thr Asp Ser Ser Ser Ser Ser
 115 120 125
 Leu Ala Leu Ile Gln Ser Ser Tyr Leu Ser Leu Asn Gln Val Thr Pro
 130 135 140
 Phe Ile Arg Phe Thr Gln Leu Thr Ala Asn Gln Ala Ile Leu Glu Ala
 145 150 155 160
 Ile Asn Gly Asn His Gln Ala Ile His Ile Val Asp Phe Asp Ile Asn
 165 170 175
 His Gly Val Gln Trp Pro Pro Leu Met Gln Ala Leu Ala Asp Arg Tyr
 180 185 190
 Pro Ala Pro Thr Leu Arg Ile Thr Gly Thr Gly Asn Asp Leu Asp Thr
 195 200 205
 Leu Arg Arg Thr Gly Asp Arg Leu Ala Lys Phe Ala His Ser Leu Gly
 210 215 220
 Leu Arg Phe Gln Phe His Pro Leu Tyr Ile Ala Asn Asn Asn His Asp
 225 230 235 240
 His Asp Glu Asp Pro Ser Ile Ile Ser Ser Ile Val Leu Leu Pro Asp
 245 250 255
 Glu Thr Leu Ala Ile Asn Cys Val Phe Tyr Leu His Arg Leu Leu Lys
 260 265 270
 Asp Arg Glu Lys Leu Arg Ile Phe Leu His Arg Val Lys Ser Met Asn
 275 280 285
 Pro Lys Ile Val Thr Ile Ala Glu Lys Glu Ala Asn His Asn His Pro
 290 295 300
 Leu Phe Leu Gln Arg Phe Ile Glu Ala Leu Asp Tyr Tyr Thr Ala Val
 305 310 315 320
 Phe Asp Ser Leu Glu Ala Thr Leu Pro Pro Gly Ser Arg Glu Arg Met
 325 330 335
 Thr Val Glu Gln Val Trp Phe Gly Arg Glu Ile Val Asp Ile Val Ala
 340 345 350
 Met Glu Gly Asp Lys Arg Lys Glu Arg His Glu Arg Phe Arg Ser Trp
 355 360 365
 Glu Val Met Leu Arg Ser Cys Gly Phe Ser Asn Val Ala Leu Ser Pro
 370 375 380
 Phe Ala Leu Ser Gln Ala Lys Leu Leu Leu Arg Leu His Tyr Pro Ser
 385 390 395 400

Glu Gly Tyr Gln Leu Gly Val Ser Ser Asn Ser Phe Phe Leu Gly Trp
405 410 415

Gln Asn Gln Pro Leu Phe Ser Ile Ser Ser Trp Arg
420 425

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTAGGGTTT CACTCCACGC

20

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TCCCCTTTT TTCCTTCTC TC

22

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTTCCCCTC AAGCCAATC

20

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA -

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGTGGCAATG TAGCTTCCAG

20

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TCGAGGCGTT GGATTATTAT AC

22

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETIC: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGCCCCATA TCTTTTTC

19

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1296 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETIC: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Solanum tuberosum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGTTAGGAT CCTTTGGTTC TTCATCATCT CAATCTCACC CTCATCATGA TGAAGAATCT

60

TCTGATCATC ATCAACGGCG TAGATTCACC GCTACTACTA CAACTATCAC CACCACCACC

120

00300: cseq0700

ACAACGACCT CACCAGCTAT TCAAATCCGC CAGCTACTCA TTAGCTGTGC GGAGTTGATT 180
 TCGCGGTCCG ATTTCTCGGC CGCGAAAAGA CTCCTTACCA TATTATCAAC TAACTCTTCT 240
 CCTTTTGGTG ATTCAACTGA ACGGTTAGTC CATCAGTTTA CTCGCGCACT TTCCCTTCGT 300
 CTCAACCGCT ATATATCGTC AACCACCAAT CATTTCATGA CACCTGTTGA AACAACTCCA 360
 ACTGATTCTT CATCTTCGTT GCCATCGTCA TCATTAGCTC TAATTCAATC ATCATATCAT 420
 TCTCTAAATC AAGTTACCCC TTTTATAAGG TTTACTCAAT TAACCGCTAA TCAAGCGATT 480
 TTAGAAGCGA TTAACGGTAA TCATCAAGCA ATCCACATCG TTGATTTCGA CATTAAATCAC 540
 GGGGTTCAAT GGCCACCGTT AATGCAAGCA CTAGCTGATC GTTACCCTGC TCCTACTCTT 600
 CGAATCACCG GTACTGGAAA TGACCTTGAT ACCCTTCGTA GAACAGGTGA TCGTTTAGCT 660
 AAATTTGCTC ACTCATTAGG GTTGAGATTT CAATTCCATC CTCTTTATAT CGCCAATAAT 720
 AACCGCGATC ACGGTGAAGA TCCTTCTATT ATTTCTCCA TTGTACTTCT CCCTGATGAA 780
 ACCCTAGCTA TCAACTGTGT TTTCTATCTC CACCGCCTTT TAAAAGACCG CGAAAAATTA 840
 AGGATTTTTT TGCATAGGGT TAAGTCAATG AACCTTAAA TTGTTACAAT CGCGGAGAAG 900
 GAAGCAAATC ATAACCATCC TCTTTTTTTA CAAAGATTTA TCGAGGCGTT GGATTATTAT 960
 ACAGCTGTGT TTGATTCATT GGAAGCTACA TTGCCACCGG GTAGTCGTGA GAGGATGACA 1020
 GTTGAACAAG TGTGGTTTGG GAGAGAAATT GTTGATATCG TGGCGATGGA AGGAGATAAA 1080
 AGGAAAGAAA GACATGAAAG GTTTAGATCA TGGGAAGTTA TGTTGAGGAG TTGTGGATTT 1140
 AGTAATGTTG CTTTAAGCCC TTTTGCATTA TCACAAGCTA AGCTTCTTTT GAGACTACAT 1200
 TATCCTTCTG AAGGCTATCA ACTCGGAGTT TCGAGTAATT CTTTCTTCTT AGGTTGGCAA 1260
 AATCAACCTC TTTTCTCCAT CTCGTCTTGG CGTTGA 1296

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Solanum tuberosum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Leu Gly Ser Phe Gly Ser Ser Ser Ser Gln Ser His Pro His His
 1 5 10 15
 Asp Glu Glu Ser Ser Asp His His Gln Arg Arg Arg Phe Thr Ala Thr
 20 25 30
 Thr Thr Thr Ile Thr Thr Thr Thr Thr Thr Thr Ser Pro Ala Ile Gln
 35 40 45

Ile Arg Gln Leu Leu Ile Ser Cys Ala Glu Leu Ile Ser Arg Ser Asp
 50 55 60
 Phe Ser Ala Ala Lys Arg Leu Leu Thr Ile Leu Ser Thr Asn Ser Ser
 65 70 75 80
 Pro Phe Gly Asp Ser Thr Glu Arg Leu Val His Gln Phe Thr Arg Ala
 85 90 95
 Leu Ser Leu Arg Leu Asn Arg Tyr Ile Ser Ser Thr Thr Asn His Phe
 100 105 110
 Met Thr Pro Val Glu Thr Thr Pro Thr Asp Ser Ser Ser Ser Leu Pro
 115 120 125
 Ser Ser Ser Leu Ala Leu Ile Gln Ser Ser Tyr His Ser Leu Asn Gln
 130 135 140
 Val Thr Pro Phe Ile Arg Phe Thr Gln Leu Thr Ala Asn Gln Ala Ile
 145 150 155 160
 Leu Glu Ala Ile Asn Gly Asn His Gln Ala Ile His Ile Val Asp Phe
 165 170 175
 Asp Ile Asn His Gly Val Gln Trp Pro Pro Leu Met Gln Ala Leu Ala
 180 185 190
 Asp Arg Tyr Pro Ala Pro Thr Leu Arg Ile Thr Gly Thr Gly Asn Asp
 195 200 205
 Leu Asp Thr Leu Arg Arg Thr Gly Asp Arg Leu Ala Lys Phe Ala His
 210 215 220
 Ser Leu Gly Leu Arg Phe Gln Phe His Pro Leu Tyr Ile Ala Asn Asn
 225 230 235 240
 Asn Arg Asp His Gly Glu Asp Pro Ser Ile Ile Ser Ser Ile Val Leu
 245 250 255
 Leu Pro Asp Glu Thr Leu Ala Ile Asn Cys Val Phe Tyr Leu His Arg
 260 265 270
 Leu Leu Lys Asp Arg Glu Lys Leu Arg Ile Phe Leu His Arg Val Lys
 275 280 285
 Ser Met Asn Pro Lys Ile Val Thr Ile Ala Glu Lys Glu Ala Asn His
 290 295 300
 Asn His Pro Leu Phe Leu Gln Arg Phe Ile Glu Ala Leu Asp Tyr Tyr
 305 310 315 320
 Thr Ala Val Phe Asp Ser Leu Glu Ala Thr Leu Pro Pro Gly Ser Arg
 325 330 335
 Glu Arg Met Thr Val Glu Gln Val Trp Phe Gly Arg Glu Ile Val Asp
 340 345 350
 Ile Val Ala Met Glu Gly Asp Lys Arg Lys Glu Arg His Glu Arg Phe
 355 360 365
 Arg Ser Trp Glu Val Met Leu Arg Ser Cys Gly Phe Ser Asn Val Ala
 370 375 380
 Leu Ser Pro Phe Ala Leu Ser Gln Ala Lys Leu Leu Leu Arg Leu His
 385 390 395 400

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Pro | Ser | Glu | Gly | Tyr | Gln | Leu | Gly | Val | Ser | Ser | Asn | Ser | Phe | Phe |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Leu | Gly | Trp | Gln | Asn | Gln | Pro | Leu | Phe | Ser | Ile | Ser | Ser | Trp | Arg | |
| | | | 420 | | | | | 425 | | | | | 430 | | |

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic DNA
- (iii) HYPOTHETIC: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

20

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic DNA
- (iii) HYPOTHETIC: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

20

(2) INFORMATION FOR SEQ ID NO: 13:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 687 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETIC: NO

(iv) ORIGINAL SOURCE:
 (A) ORGANISM: Arabidopsis thaliana

(vi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
```

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GAGAGGTCAT | CAAACCCTAG | CAGTCCACCT | CCATCTCTCC | GCATAACCGG | ATGCGGTCGA | 60  |
| GATGTAACCG | GATTAAACCG | AACTGGAGAC | CGGTAAACCC | GGTTCGCTGA | CTCTTTAGGT | 120 |
| CTCCAATTCC | AGTTTCACAC | GCTAGTGATC | GTAGAAGAAG | ATCTCGCCGG | ACTTTTGCTA | 180 |



CAGATCCGAT TGTTAGCTCT CTCAGCCGTA CAAGGAGAGA CCATTGCCGT CAATTGTGTT 240  
 CACTTCCTCC AAAAAATATT TAACGACGAT GGAGATATGA TCGGTCACCT CTTGTCAGCG 300  
 ATCAAGAGCT TAAACTCTAG AATCGTTACA ATGGCAGAGA GAGAAGCTAA TCATGGAGAT 360  
 CACTCGTTCT TGAATAGATT CTCTGAGGCA GTGGATCATT ACATGGCGAT CTTTGATTCTG 420  
 TTGGAAGCGA CGTTGCCGCC AAATAGCCGA GAGAGACTAA CCCTAGAGCA ACGGTGGTTC 480  
 GGTAAGGAGA TTTTGGATGT TGTGGCGGCG GAAGAGACGG AGAGAAAGCA AAGACATCGG 540  
 AGGTTTGAGA TTTGGGAAGA GATGATGAAG AGGTTTGGTT TCGTTAACGT TCCTATTGGA 600  
 AGCTTTGCTT TGTCTCAAGC TAAGCTTCTT CTTAGACTTC ATTATCCTTC AGAAGGTTAT 660  
 AATCTTCAGT TCCTTAACAA TTCTTTG 687

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Arg | Ser | Ser | Asn | Pro | Ser | Ser | Pro | Pro | Pro | Ser | Leu | Arg | Ile | Thr | 1   | 5   | 10  | 15  |
| Gly | Cys | Gly | Arg | Asp | Val | Thr | Gly | Leu | Asn | Arg | Thr | Gly | Asp | Arg | Leu | 20  | 25  | 30  |     |
| Thr | Arg | Phe | Ala | Asp | Ser | Leu | Gly | Leu | Gln | Phe | Gln | Phe | His | Thr | Leu | 35  | 40  | 45  |     |
| Val | Ile | Val | Glu | Glu | Asp | Leu | Ala | Gly | Leu | Leu | Leu | Gln | Ile | Arg | Leu | 50  | 55  | 60  |     |
| Leu | Ala | Leu | Ser | Ala | Val | Gln | Gly | Glu | Thr | Ile | Ala | Val | Asn | Cys | Val | 65  | 70  | 75  | 80  |
| His | Phe | Leu | His | Lys | Ile | Phe | Asn | Asp | Asp | Gly | Asp | Met | Ile | Gly | His | 85  | 90  | 95  |     |
| Phe | Leu | Ser | Ala | Ile | Lys | Ser | Leu | Asn | Ser | Arg | Ile | Val | Thr | Met | Ala | 100 | 105 | 110 |     |
| Glu | Arg | Glu | Ala | Asn | His | Gly | Asp | His | Ser | Phe | Leu | Asn | Arg | Phe | Ser | 115 | 120 | 125 |     |
| Glu | Ala | Val | Asp | His | Tyr | Met | Ala | Ile | Phe | Asp | Ser | Leu | Glu | Ala | Thr | 130 | 135 | 140 |     |
| Leu | Pro | Pro | Asn | Ser | Arg | Glu | Arg | Leu | Thr | Leu | Glu | Gln | Arg | Trp | Phe | 145 | 150 | 155 | 160 |

005070-0902000

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Lys | Glu | Ile | Leu | Asp | Val | Val | Ala | Ala | Glu | Glu | Thr | Glu | Arg | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Arg | His | Arg | Arg | Phe | Glu | Ile | Trp | Glu | Glu | Met | Met | Lys | Arg | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Phe | Val | Asn | Val | Pro | Ile | Gly | Ser | Phe | Ala | Leu | Ser | Gln | Ala | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Leu | Leu | Arg | Leu | His | Tyr | Pro | Ser | Glu | Gly | Tyr | Asn | Leu | Gln | Phe |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Asn | Asn | Ser | Leu |     |     |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

005070" 09000000